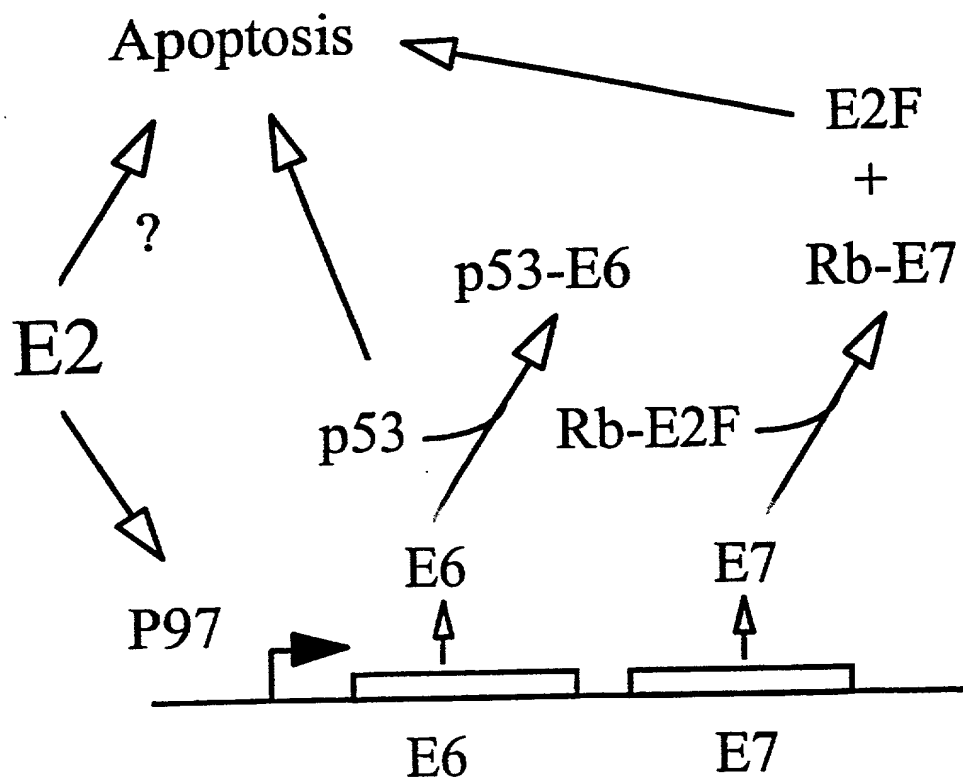


Fig. 1

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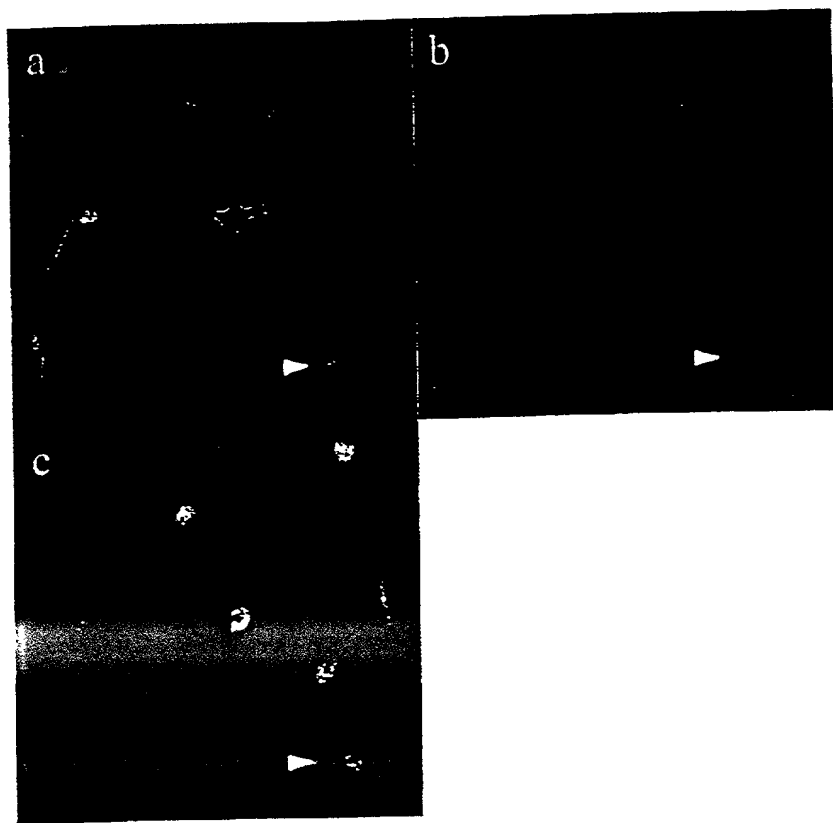
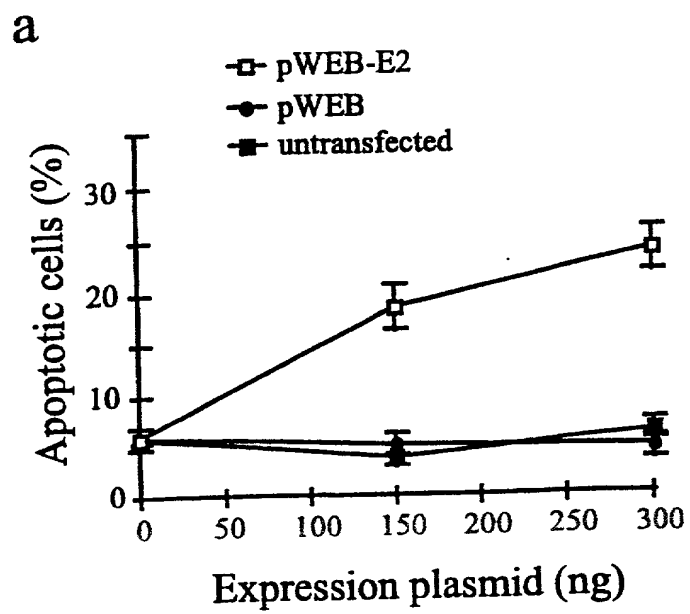


Fig. 2

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Fig. 3A



b

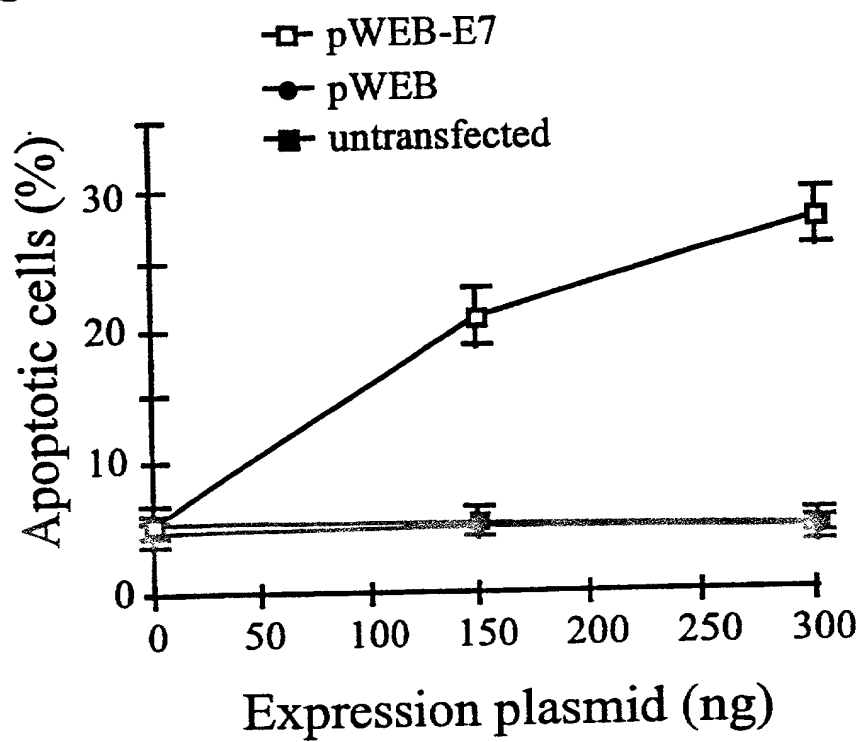


Fig. 3B

Fig. 4

a

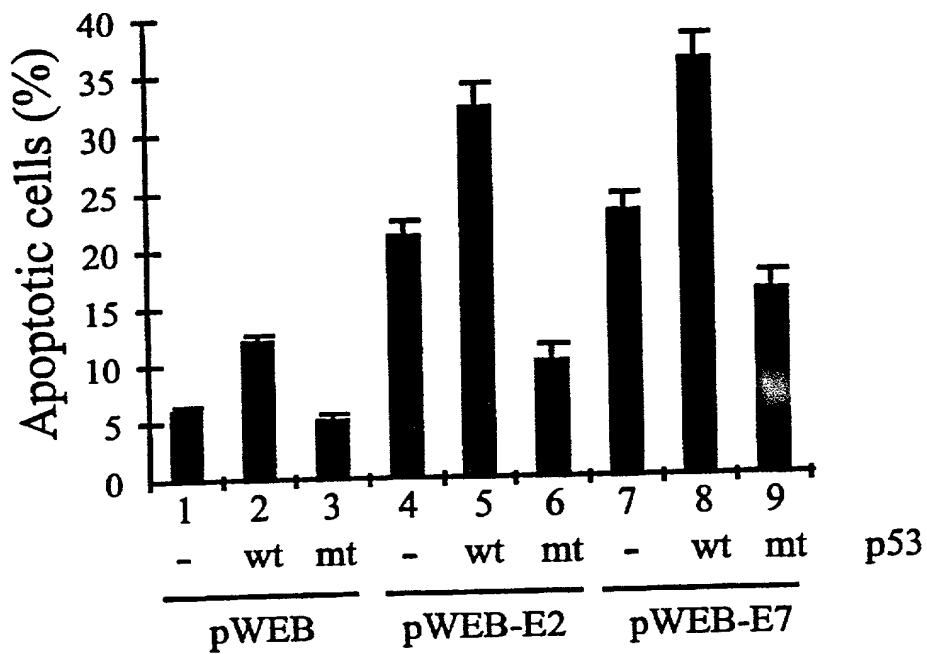


Fig. 4B

b

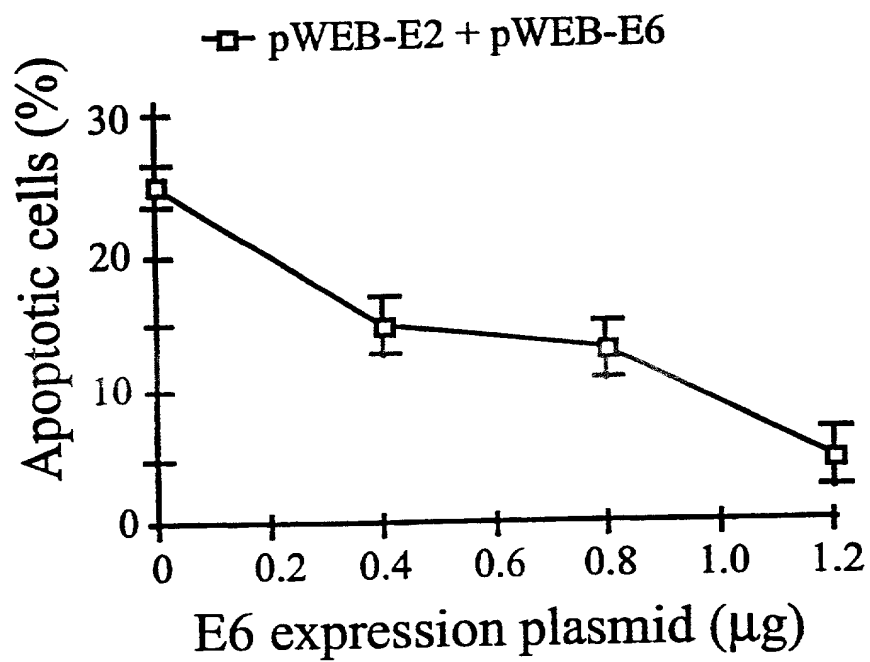
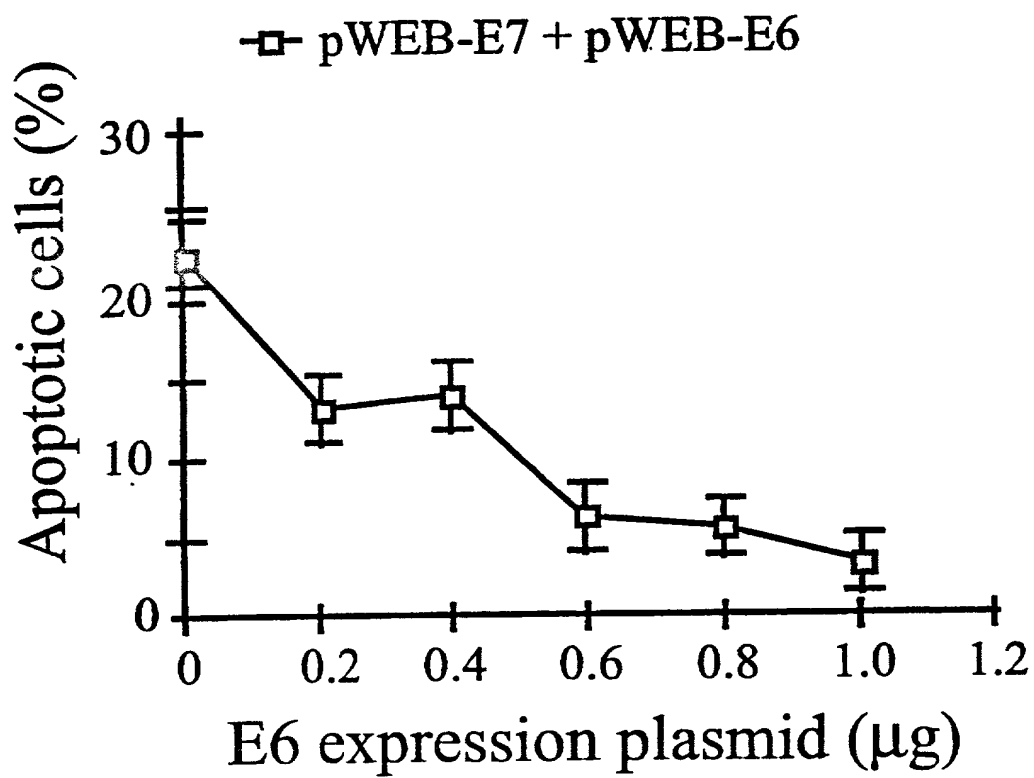


Fig 4C

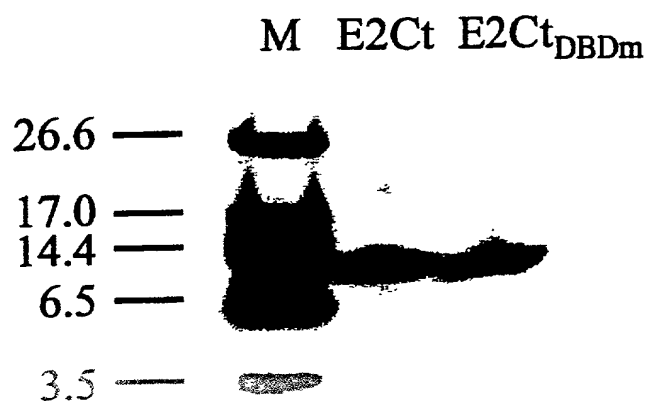
C



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Fig 5A

a



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Fig 5B

b

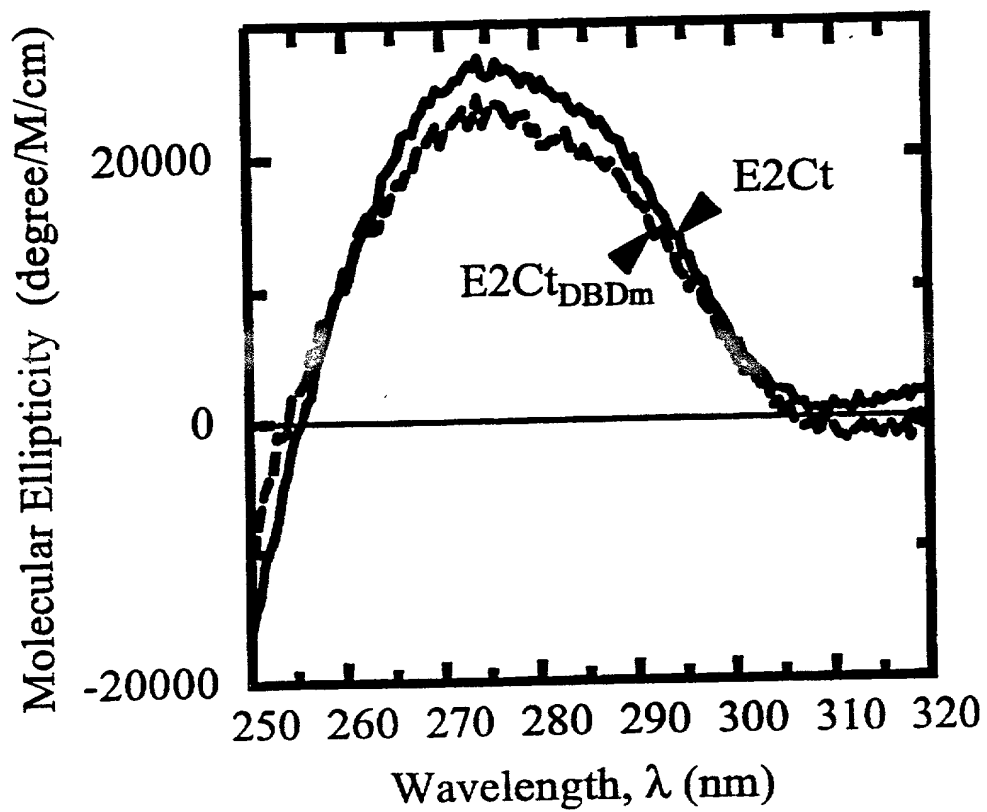


Fig 5C

C

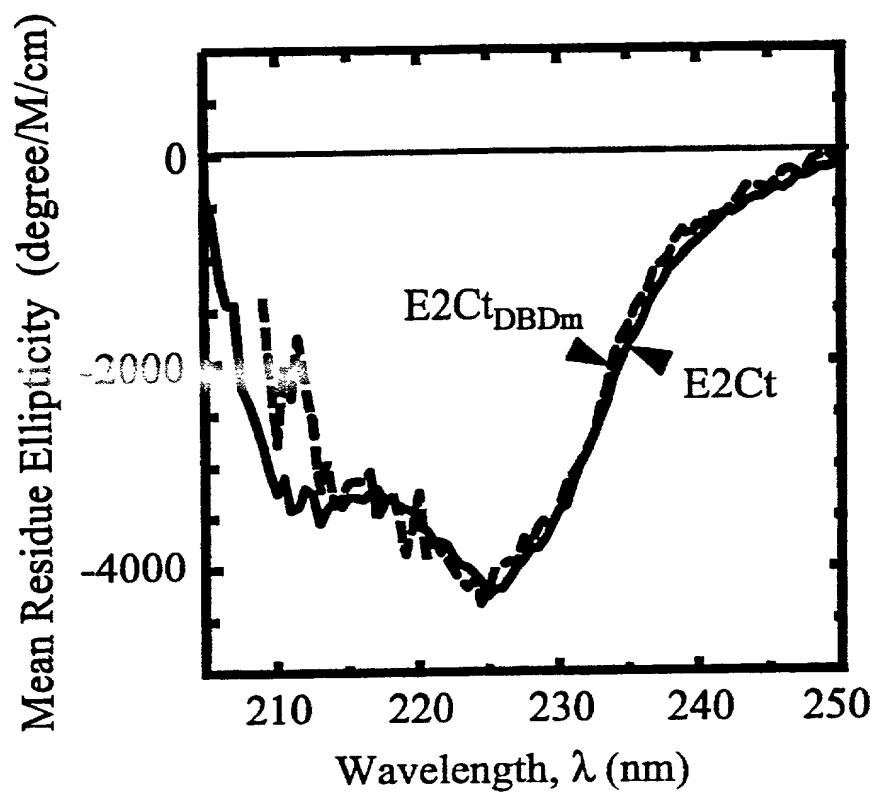
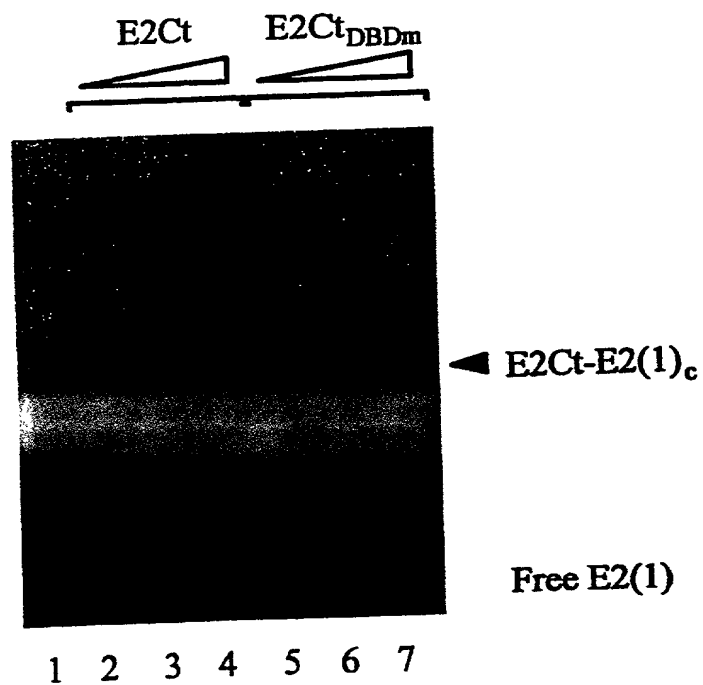


Fig 5D

d



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Fig. 6

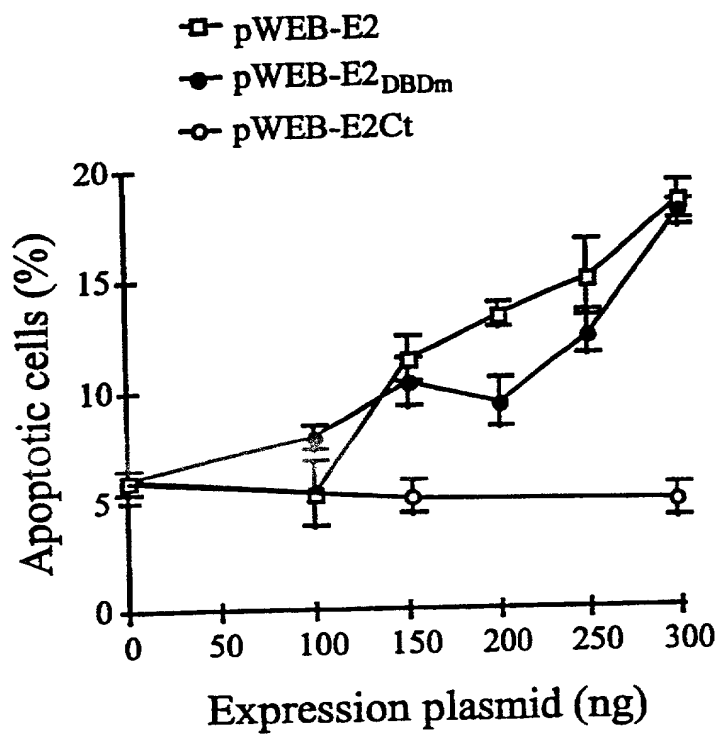
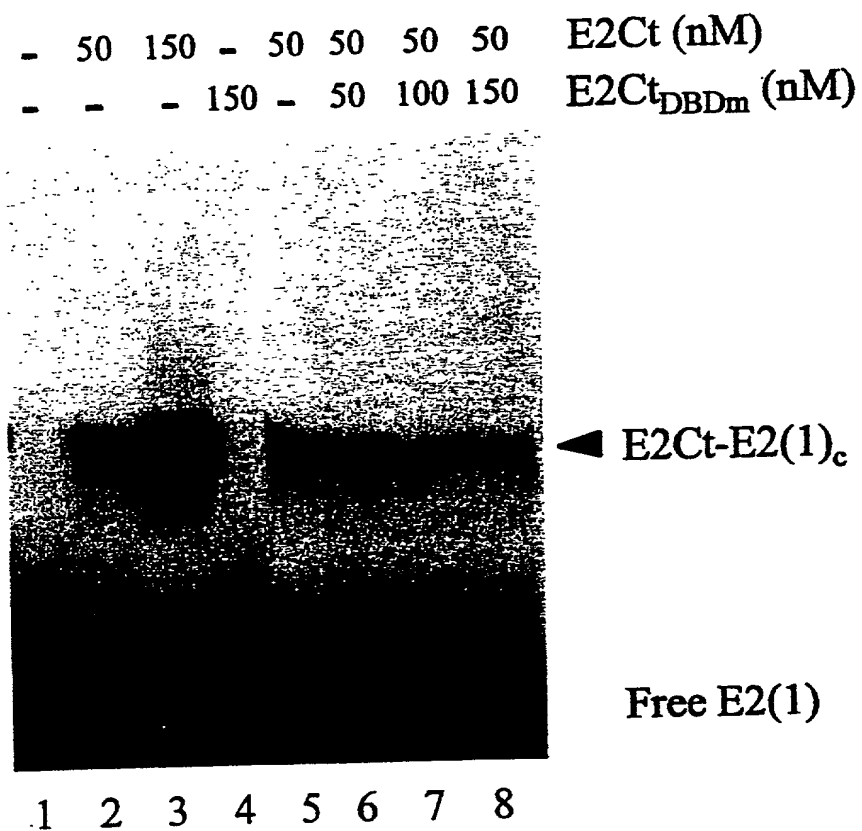


Fig. 7A

a



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Fig. 7B

b

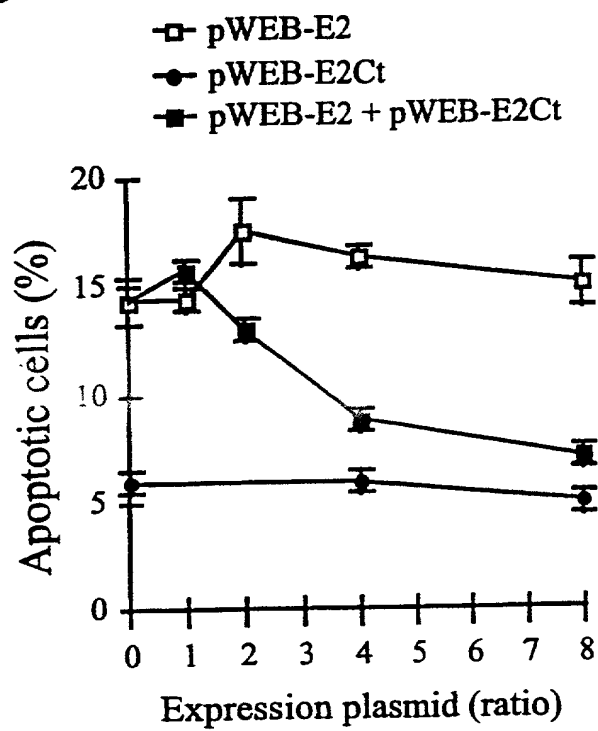


Fig. 8

The E2 proteins used in this work

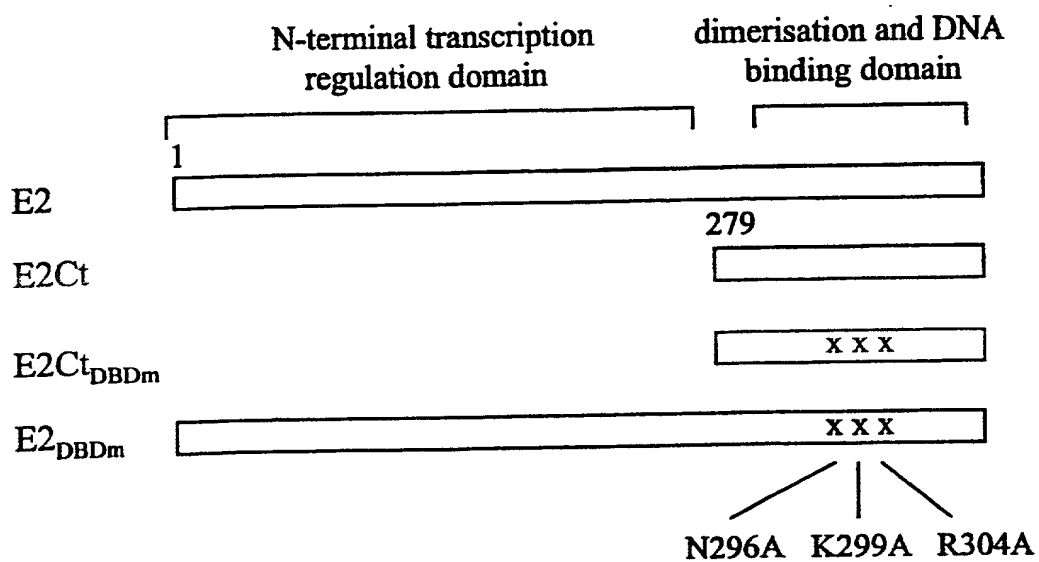


Fig. 9

HPV 16 E2

2755 ATGGGAGACTCTTTGCCAACGTTTAAATGTGTGTCAGGACAAAATACTAACACATTATGAA
-----+-----+-----+-----+-----+-----+-----
M E T L C Q R L N V C Q D K I L T H Y E

2815 AATGATAGTACAGACCTACGTGACCATATAGACTATTGGAAACACATGCGCCTAGAATGT
-----+-----+-----+-----+-----+-----+-----
N D S T D L R D H I D Y W K H M R L E C

GCTATTTATTACAAGGCCAGAGAAATGGGATTTAAACATATTAACCACCAAGTGGTGCCA

2875 -----+-----+-----+-----+-----+-----+-----
A I Y Y K A R E M G F K H I N H Q V V P

2935 ACACTGGCTGTATCAAAGAATAAAGCATTACAAGCAATTGAACTGCAACTAACGTTAGAA
-----+-----+-----+-----+-----+-----+-----
T L A V S K N K A L Q A I E L Q L T L E

2995 ACAATATATAACTCACAATATAGTAATGAAAAGTGGACATTACAAGACGTTAGCCTTGAA
-----+-----+-----+-----+-----+-----+-----
T I Y N S Q Y S N E K W T L Q D V S L E

3055 GTGTATTTAACTGCACCAACAGGATGTATAAAAAACATGGATATACAGTGAAGTGCAG
-----+-----+-----+-----+-----+-----+-----
V Y L T A P T G C I K K H G Y T V E V Q

3115 TTTGATGGAGACATATGCAATACAATGCATTATACAAACTGGACACATATATATATTTGT
-----+-----+-----+-----+-----+-----+-----
F D G D I C N T M H Y T N W T H I Y I C

3175 GAAGAAGCATCAGTAACTGTGGTAGAGGGTCAAGTTGACTATTATGGTTTATATTATGTT
-----+-----+-----+-----+-----+-----+-----
E E A S V T V V E G Q V D Y Y G L Y Y V

3235 CATGAAGGAATACGAACATATTTTGTGCAGTTTAAAGATGATGCAGAAAAATATAGTAAA
-----+-----+-----+-----+-----+-----+-----
H E G I R T Y F V Q F K D D A E K Y S K

3295 AATAAAGTATGGGAAGTTCATGCGGGTGGTCAGGTAATATTATGTCCTACATCTGTGTTT
-----+-----+-----+-----+-----+-----+-----
N K V W E V H A G G Q V I L C P T S V F

3355 AGCAGCAACGAAGTATCCTCTCCTGAAATTATTAGGCAGCACTTGGCCAACCACCCCGCC
-----+-----+-----+-----+-----+-----+-----
S S N E V S S P E I I R Q H L A N H P A

3415 GCGACCCATACCAAAGCCGTCGCCCTTGGGCACCGAAGAAACACAGACGACTATCCAGCGA
-----+-----+-----+-----+-----+-----+-----

10047990.01402

A T H T K A V A L G T E E T Q T T I Q R

3475 CCAAGATCAGAGCCAGACACCGGAAACCCCTGCCACACCACTAAGTTGTTGCACAGAGAC
-----+-----+-----+-----+-----+-----+-----
P R S E P D T G N P C H T T K L L H R D

3535 TCAGTGGACAGTGCTCCAATCCTCACTGCATTTAACAGCTCACACAAAGGACGGATTAAC
-----+-----+-----+-----+-----+-----+-----
S V D S A P I L T A F N S S H K G R I N

3595 TGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTAATACTTTAAATGT
-----+-----+-----+-----+-----+-----+-----
C N S N T T P I V H L K G D A N T L K C

3655 TTAAGATATAGATTTAAAAAGCATTGTACATTGTATACTGCAGTGTCTGCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----
L R Y R F K K H C T L Y T A V S S T W H

3715 TGGACAGGACATAATGTAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

3775 TGGCAACGTGACCAATTTTTGTCTCAAGTTAAAATACCAAAAACCTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

3835 GGATTTATGTCTATATGA
-----+-----+----- 3852
G F M S I * -

204 FT0 "066403T

Fig 10

HPV 16 E2DBDm

ATGGAGACTCTTTGCCAACGTTTAAATGTGTGTGCAGGACAAAATACTAACACATTATGAA
2755 -----+-----+-----+-----+-----+-----+-----+
M E T L C Q R L N V C Q D K I L T H Y E

AATGATAGTAGACACCTACGTGACCATATAGACTATTGGAAACACATGCGCCTAGAATGT
2815 -----+-----+-----+-----+-----+-----+-----+
N D S T D L R D H I D Y W K H M R L E C

GCTATTTATTACAAGGCCAGAGAAATGGGATTTAAACATATTAACCACCAAGTGGTGCCA
2875 -----+-----+-----+-----+-----+-----+-----+
A I Y Y K A R E M G F K H I N H Q V V P

ACACTGGCTGTATCAAAGAATAAAGCATTACAAGCAATTGAACTGCAACTAACGTTAGAA
2935 -----+-----+-----+-----+-----+-----+-----+
T L A V S K N K A L Q A I E L Q L T L E

ACAATATATAACTCACAAATATAGTAATGAAAAGTGGACATTACAAGACGTTAGCCTTGAA
2995 -----+-----+-----+-----+-----+-----+-----+
T I Y N S Q Y S N E K W T L Q D V S L E

GTGTATTTAACTGCACCAACAGGATGTATAAAAAACATGGATATACAGTGAAGTGCAG
3055 -----+-----+-----+-----+-----+-----+-----+
V Y L T A P T G C I K K H G Y T V E V Q

TTTGATGGAGACATATGCAATACAATGCATTATACAAACTGGACACATATATATATTGT
3115 -----+-----+-----+-----+-----+-----+-----+
F D G D I C N T M H Y T N W T H I Y I C

GAAGAAGCATCAGTAAGTGTGGTAGAGGGTCAAGTTGACTATTATGGTTTTATATTATGTT
3175 -----+-----+-----+-----+-----+-----+-----+
E E A S V T V V E G Q V D Y Y G L Y Y V

CATGAAGGAATACGAACATATTTTGTGCAGTTTAAAGATGATGCAGAAAAATATAGTAAA
3235 -----+-----+-----+-----+-----+-----+-----+
H E G I R T Y F V Q F K D D A E K Y S K

AATAAAGTATGGGAAGTTCATGCGGGTGGTCAGGTAATATTATGTCCTACATCTGTGTTT
3295 -----+-----+-----+-----+-----+-----+-----+
N K V W E V H A G G Q V I L C P T S V F

AGCAGCAACGAAGTATCCTCTCCTGAAATTATTAGGCAGCACTTGGCCAACCACCCCGCC
3355 -----+-----+-----+-----+-----+-----+-----+
S S N E V S S P E I I R Q H L A N H P A

GCGACCCATACCAAAGCCGTCGCCTTGGGCACCGAAGAAACACAGACGACTATCCAGCGA
3415 -----+-----+-----+-----+-----+-----+-----+
A T H T K A V A L G T E E T Q T T I O R

3475 CCAAGATCAGAGCCAGACACCGGAAACCCCTGCCACACCACTAAGTTGTTGCACAGAGAC
-----+-----+-----+-----+-----+-----+-----
P R S E P D T G N P C H T T K L L H R D

3535 TCAGTGGACAGTGCTCCAATCCTCACTGCATTTAACAGCTCACACAAAGGACGGATTAAAC
-----+-----+-----+-----+-----+-----+-----
S V D S A P I L T A F N S S H K G R I N

3595 TGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTgctACTTTAgcaTGT
-----+-----+-----+-----+-----+-----+-----
C N S N T T P I V H L K G D A A T L A C

3655 TTAAGATATgcaTTTAAAAGCATTGTACATTGTATACTGCAGTGTCTGTCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----
L R Y A F K K H C T L Y T A V S S T W H

3715 TGGACAGGACATAATGTAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

3775 TGGCAACGTGACCAATTTTGTCTCAAGTTAAAATACCAAAAACATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

3835 GGATTTATGTCTATATGA
-----+-----+----- 3852
G F M S I * -

204740 06624007

Fig 11

E2Ct

ATGAACTGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTAATACTTTAAAATGT
-----+-----+-----+-----+-----+-----+-----+-----
M N C N S N T T P I V H L K G D A N T L K C

TTAAGATATAGATTTAAAAGCATTGTACATTGTATACTGCAGTGTCTGCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----+-----
L R Y R F K K H C T L Y T A V S S T W H

TGGACAGGACATAATGTAAACATAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----+-----
W T G H N V K H K S A I V T L T Y D S E

TGGCAACGTGACCAATTTTTGTCTCAAGTTAAAATACCAAAAACTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----+-----
W Q R D Q F L S Q V K I P K T I T V S T

GGATTATGTCTATATGA
-----+-----+----- 3852
G F M S I * -

2044710 0664400

Fig 12

E2CtDBDm

```
ATGAACTGTAATAGTAACACTACACCCATAGTACATTTAAAAGGTGATGCTgctACTTTAgcaTGT
-----+-----+-----+-----+-----+-----+-----+-----+-----+
M N C N S N T T P I V H L K G D A A T L A C

TTAAGATATgcaTTTAAAAAGCATTGTACATTGTATACTGCAGTGTCTGTCTACATGGCAT
-----+-----+-----+-----+-----+-----+-----+-----+-----+
L R Y A F K K H C T L Y T A V S S T W H

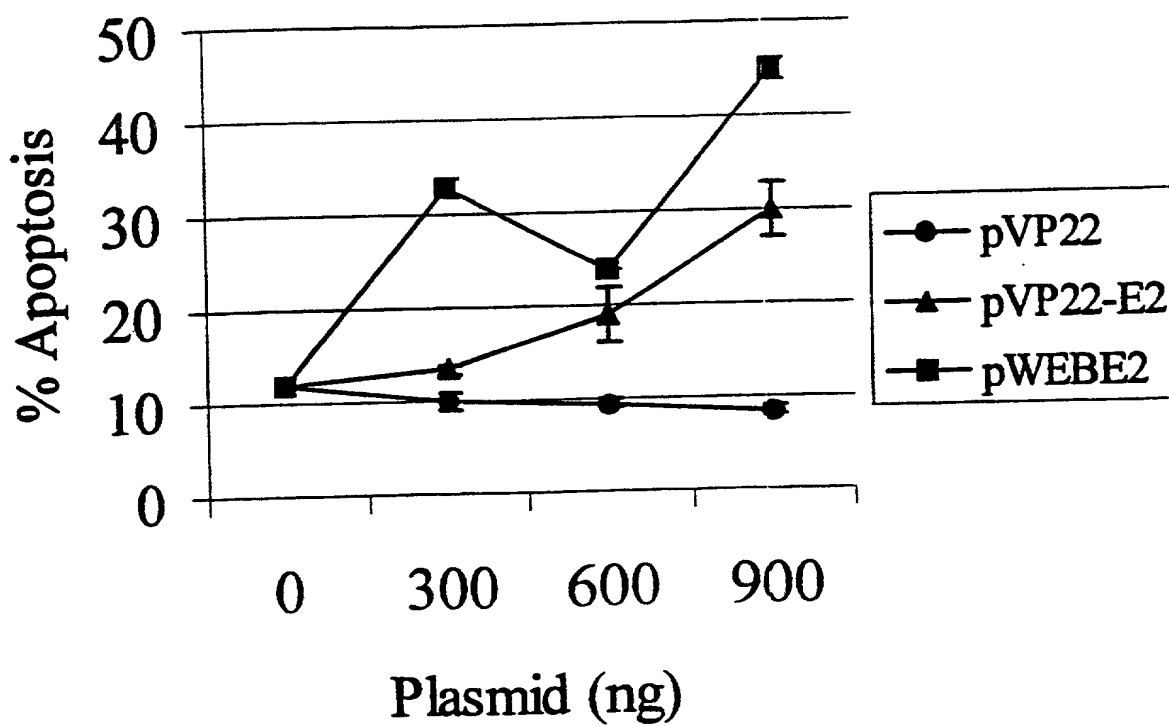
TGGACAGGACATAATGTAAACATAAAAAGTGCAATTGTTACACTTACATATGATAGTGAA
-----+-----+-----+-----+-----+-----+-----+-----+-----+
W T G H N V K H K S A I V T L T Y D S E

TGGCAACGTGACCAATTTTGTCTCAAGTTAAATACCAAAAACACTATTACAGTGTCTACT
-----+-----+-----+-----+-----+-----+-----+-----+-----+
W Q R D Q F L S Q V K I P K T I T V S T

GGATTTATGTCTATATGA
-----+-----+-----+-----+-----+-----+-----+-----+-----+
G F M S I * - 3852
```

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Fig 13



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